

17th EURO BIOTECHNOLOGY CONGRESS

September 25-27, 2017 Berlin, Germany

Identification and cytogenetic characteristics of oat DH lines obtained by wide crossing with maize

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One of the most effective ways to generate oat DH lines is to perform a wide crossing with maize. An elevated level of homozygosity possessed by DH lines is a feature desirable for the durability of certain characteristics of new autogamous cultivars. Unlike other cereals, oat can form stable and fertile partial hybrids after pollinating with maize, since oat is able to retain one or more maize chromosomes without a lethal effect. The identification of an oat-maize addition lines could help in the selection of partial hybrids and describing the impact of additional chromosomes on the morphological and agricultural features of oat. The aim of the study was to detect maize DNA introgression into the oat genome using the PCR technique. To establish whether maize genomic DNA was present in oat DH lines, a fragment of maize-specific retro-transposon Grande1 (500 bp) was amplified and was detected after an electrophoresis in an agarose gel. All DH lines with detected fragments of retro-transposon Grande1 were analyzed with genomic in situ hybridization to detect and visualize maize chromosomes. Among the 94 oat DH lines that were obtained, 47 retained the maize chromatin, as inferred from the presence of a fragment of the Grande1 retro-transposon. Fertile lines that produced grains underwent GISH analysis, which revealed from 1 to 4 maize additional chromosomes. Aside from whole maize chromosomes, a banding pattern was also observed in most cases, which presumably co-localized with 25S rDNA sites. Additional hybridization signals were detected in 2-3 chromosome pairs depending on the analyzed line. These signals might correspond to oat's 5S rDNA sites, although it cannot be eliminated that these sequences originated from the maize genome and were inserted into oat chromosomes.

Acknowledgement: Research funded by National Centre for Research and Development, No. PBS3/B8/17/2015

Biography

Tomasz Warzecha has completed his PhD in 2001 from Agricultural University in Kraków, Poland. He has participated at the International Postgraduate Course on Biotechnology in Agriculture, Plants and Microorganisms at the Hebrew University of Jerusalem. Additionally completed the Pedagogical Studium, majored in Biology and Chemistry at Jagiellonian University in Krakow, Poland. He has worked in a project focused to examine natural variation in the recombination pathways in maize at the Department of Plant Breeding and Genetics at Cornell University, Ithaca, USA.

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